

Quiz

Chapter 10

Bioinformatics

Full Marks: 10

Time: 10 min

1. The activity of a protein is related with

- a) Gene sequence of the protein b) Amino acid sequence of the protein c) Both of these
d) None of these

2. The amino acid sequence of a protein can be retrieved from

- a) Expasy b) SWISS PDB c) PDB d) NCBI

3. Identification of a gene or protein can be retrieved by sequence alignment with known gene/proteins. This could be done by

- a) BLAST b) Homology Modeling c) SWISS-PROT d) Clustal W

4. Homology modeling of a protein may be done by the following:

- a) CASTp b) LigASite c) SWISS MODEL d) PSI BLAST

5. One gene can lead to a particular protein, but a protein can lead to multiple genes- The statement is

- a) TRUE b) FALSE c) Can not be said-depends on case to case

6. The sequence alignment may be done with

- a) Gene Bank format b) FASTA Format c) Python format d) .txt format

7. The amino acid substitution in a protein can be tracked by

- a) sequence alignment with BLAST b) sequence alignment with CLUSTAL W c) Sequence alignment with BoxShade
d) All of these

8. If a receptor structure is unknown, still the docking between the receptor and ligand can be performed. The statement is true IF

- a) the sequence of the protein is known b) the sequence of the protein is unknown c) the biological activity of the protein is known
d) the statement can not be true

9. Homology modeling of a protein requires

- a) template proteins with high percentage similarity b) template proteins with low percentage similarity
c) template proteins with same binding sites d) both a and c e) both b and c

10. The hydrophathicity (hydrophobicity) of a protein can be measured by

- a) GRAVY index b) π index c) Ramachandran Plot d) σ - π plot